#8

RAW SEQUENCE LISTING   DATE: 04/30/2001
PATENT APPLICATION: US/09/403,269   TIME: 13:57:00

Input Set : A:\Pto.amc
Output Set: N:\CRF3\04302001\I403269.raw

```
  3 <110> APPLICANT: ULF, Lindahl
  4        LI, Jin-Ping
  6 <120> TITLE OF INVENTION: DNA Sequence Coding for a Mammalian Glucuronyl C5-Epimerase and a
  7        Process for Its Production
  9 <130> FILE REFERENCE: 003300-589
 11 <140> CURRENT APPLICATION NUMBER: US 09/403,269
 12 <141> CURRENT FILING DATE: 1999-10-18
 14 <150> PRIOR APPLICATION NUMBER: SE 9701454-2
 15 <151> PRIOR FILING DATE: 1997-04-18
 17 <150> PRIOR APPLICATION NUMBER: PCT/SE98/00703
 18 <151> PRIOR FILING DATE: 1998-04-17
 20 <160> NUMBER OF SEQ ID NOS: 13
 22 <170> SOFTWARE: PatentIn version 3.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 17
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Human
 30 <400> SEQUENCE: 1
 31 gctgattctt ttctgtc                                              17
 34 <210> SEQ ID NO: 2
 35 <211> LENGTH: 13
 36 <212> TYPE: PRT
 37 <213> ORGANISM: Human
 39 <220> FEATURE:
 40 <221> NAME/KEY: PEPTIDE
 41 <222> LOCATION: (5)..(5)
 42 <223> OTHER INFORMATION: Amino acid 5 is Xaa wherein Xaa = any amino acid.
 44 <400> SEQUENCE: 2
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W--> 46 Pro Asn Asp Trp Xaa Val Pro Lys Gly Cys Phe Met Ala
```
 47 1              5                   10
 49 <210> SEQ ID NO: 3
 50 <211> LENGTH: 11
 51 <212> TYPE: PRT
 52 <213> ORGANISM: Human
 54 <220> FEATURE:
 55 <221> NAME/KEY: PEPTIDE
 56 <222> LOCATION: (2)..(10)
 57 <223> OTHER INFORMATION: Amino acids 2 and 10 are Xaa wherein Xaa = any amino acid.
 59 <400> SEQUENCE: 3
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W--> 61 Pro Xaa Asp Trp Thr Val Pro Lys Gly Xaa Phe
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 62 1              5                   10
 64 <210> SEQ ID NO: 4
 65 <211> LENGTH: 8
 66 <212> TYPE: PRT
 67 <213> ORGANISM: Human
 69 <220> FEATURE:
 70 <221> NAME/KEY: PEPTIDE
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```
   71 <222> LOCATION: (4)..(4)
   72 <223> OTHER INFORMATION: Amino acid 4 is Xaa wherein Xaa = any amino acid.
   74 <400> SEQUENCE: 4
W--> 76 Pro Asn Asp Xaa Thr Val Pro Lys
   77 1               5
   79 <210> SEQ ID NO: 5
   80 <211> LENGTH: 15
   81 <212> TYPE: PRT
   82 <213> ORGANISM: Human
   84 <220> FEATURE:
   85 <221> NAME/KEY: PEPTIDE
   86 <222> LOCATION: (1)..(11)
   87 <223> OTHER INFORMATION: Amino acids 1, 2 and 11 are Xaa wherein Xaa = any amino acid.
   89 <400> SEQUENCE: 5
W--> 91 Xaa Xaa Ile Ala Pro Glu Thr Ser Glu Gly Xaa Ser Leu Gln Leu
   92 1               5                  10                 15
   94 <210> SEQ ID NO: 6
   95 <211> LENGTH: 10
   96 <212> TYPE: PRT
   97 <213> ORGANISM: Human
   99 <400> SEQUENCE: 6
  101 Gly Gly Trp Pro Ile Met Val Thr Arg Lys
  102 1               5                  10
  104 <210> SEQ ID NO: 7
  105 <211> LENGTH: 8
  106 <212> TYPE: PRT
  107 <213> ORGANISM: Human
  109 <400> SEQUENCE: 7
  111 Phe Leu Ser Glu Gln His Gly Val
  112 1               5
  114 <210> SEQ ID NO: 8
  115 <211> LENGTH: 36
  116 <212> TYPE: PRT
  117 <213> ORGANISM: Human
  119 <220> FEATURE:
  120 <221> NAME/KEY: PEPTIDE
  121 <222> LOCATION: (30)..(30)
  122 <223> OTHER INFORMATION: Amino acid 30 is Xaa wherein Xaa = any amino acid.
  124 <400> SEQUENCE: 8
  126 Lys Ala Met Leu Pro Leu Tyr Asp Thr Gly Ser Gly Thr Ile Tyr Asp
  127 1               5                  10                 15
W--> 129 Leu Arg His Phe Met Leu Gly Ile Ala Pro Asn Leu Ala Xaa Trp Asp
  130            20                 25                 30
  132 Tyr His Thr Thr
  133            35
  135 <210> SEQ ID NO: 9
  136 <211> LENGTH: 25
  137 <212> TYPE: DNA
  138 <213> ORGANISM: Human
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```
W--> 139 <220> FEATURE:
     140 <221> NAME/KEY: misc_feature
     141 <222> LOCATION: (14)..(23)
     142 <223> OTHER INFORMATION: Nucleotides 14, 20 and 23 are "n" wherein "n" = any
     143       nucleotide.
     145 <400> SEQUENCE: 9
W--> 146 ccgaattcaa rgcnatgytn ccnyt                                        25
     149 <210> SEQ ID NO: 10
     150 <211> LENGTH: 26
     151 <212> TYPE: DNA
     152 <213> ORGANISM: Human
     154 <220> FEATURE:
     155 <221> NAME/KEY: misc_feature
     156 <222> LOCATION: (14)..(17)
     157 <223> OTHER INFORMATION: Nucleotides 14 and 17 are "n" wherein "n" = any nucleotide.
     159 <400> SEQUENCE: 10
W--> 160 ccgaattcga yytnmgncay ttyatg                                      26
     163 <210> SEQ ID NO: 11
     164 <211> LENGTH: 25
     165 <212> TYPE: DNA
     166 <213> ORGANISM: Human
     168 <220> FEATURE:
     169 <221> NAME/KEY: misc_feature
     170 <222> LOCATION: (11)..(11)
     171 <223> OTHER INFORMATION: Nucleotide 11 is "n" wherein "n" = any nucleotide.
     173 <400> SEQUENCE: 11
W--> 174 ccggatccgt ngtrtgrtar tccca                                       25
     177 <210> SEQ ID NO: 12
     178 <211> LENGTH: 3085
     179 <212> TYPE: DNA
     180 <213> ORGANISM: Human
     182 <220> FEATURE:
     183 <221> NAME/KEY: CDS
     184 <222> LOCATION: (73)..(1404)
     186 <400> SEQUENCE: 12
     187 tccaagctga attctcatag ctattccaaa gtctatgcac agagagcccc ttatcaccct       60
     189 gatggtgtgt tt atg tcc ttt gaa ggc tac aat gtg gaa gtc cga gac aga      111
     190               Met Ser Phe Glu Gly Tyr Asn Val Glu Val Arg Asp Arg
     191                1               5                  10
     193 gtc aag tgc ata agt ggg gtt gaa ggt gta cct tta tct aca cag tgg       159
     194 Val Lys Cys Ile Ser Gly Val Glu Gly Val Pro Leu Ser Thr Gln Trp
     195     15                  20                  25
     197 gga cct caa ggc tat ttc tac cca atc cag att gca cag tat ggg tta       207
     198 Gly Pro Gln Gly Tyr Phe Tyr Pro Ile Gln Ile Ala Gln Tyr Gly Leu
     199 30                  35                  40                  45
     201 agt cac tac agc aag aat cta act gaa aaa ccc cct cat ata gag gta       255
     202 Ser His Tyr Ser Lys Asn Leu Thr Glu Lys Pro Pro His Ile Glu Val
     203             50                  55                  60
     205 tat gaa aca gca gaa gac agg gac aaa aac agc aag ccc aat gac tgg       303
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```
206 Tyr Glu Thr Ala Glu Asp Arg Asp Lys Asn Ser Lys Pro Asn Asp Trp
207             65              70              75
209 act gtg ccc aag ggc tgc ttt atg gct agt gtg gct gat aag tca aga       351
210 Thr Val Pro Lys Gly Cys Phe Met Ala Ser Val Ala Asp Lys Ser Arg
211             80              85              90
213 ttc acc aat gtt aaa cag ttc att gct cca gaa acc agt gaa ggt gta       399
214 Phe Thr Asn Val Lys Gln Phe Ile Ala Pro Glu Thr Ser Glu Gly Val
215             95              100             105
217 tcc ttg caa ctg ggg aac aca aaa gat ttt att att tca ttt gac ctc       447
218 Ser Leu Gln Leu Gly Asn Thr Lys Asp Phe Ile Ile Ser Phe Asp Leu
219 110             115             120             125
221 aag ttc tta aca aat gga agc gtg tct gtg gtt ctg gag acg aca gaa       495
222 Lys Phe Leu Thr Asn Gly Ser Val Ser Val Val Leu Glu Thr Thr Glu
223             130             135             140
225 aag aat cag ctc ttc act gta cat tat gtc tca aat acc cag cta att       543
226 Lys Asn Gln Leu Phe Thr Val His Tyr Val Ser Asn Thr Gln Leu Ile
227             145             150             155
229 gct ttt aaa gaa aga gac ata tac tat ggc atc ggg ccc aga aca tca       591
230 Ala Phe Lys Glu Arg Asp Ile Tyr Tyr Gly Ile Gly Pro Arg Thr Ser
231             160             165             170
233 tgg agc aca gtt acc cgg gac ctg gtc act gac ctc agg aaa gga gtg       639
234 Trp Ser Thr Val Thr Arg Asp Leu Val Thr Asp Leu Arg Lys Gly Val
235             175             180             185
237 ggt ctt tcc aac aca aaa gct gtc aag cca aca aga ata atg ccc aag       687
238 Gly Leu Ser Asn Thr Lys Ala Val Lys Pro Thr Arg Ile Met Pro Lys
239 190             195             200             205
241 aag gtg gtt agg ttg att gcg aaa ggg aag ggc ttc ctt gac aac att       735
242 Lys Val Val Arg Leu Ile Ala Lys Gly Lys Gly Phe Leu Asp Asn Ile
243             210             215             220
245 acc atc tct acc aca gcc cac atg gct gcc ttc ttc gct gcc agt gac       783
246 Thr Ile Ser Thr Thr Ala His Met Ala Ala Phe Phe Ala Ala Ser Asp
247             225             230             235
249 tgg ctg gtg agg aac cag gat gag aaa ggc ggc tgg ccg att atg gtg       831
250 Trp Leu Val Arg Asn Gln Asp Glu Lys Gly Gly Trp Pro Ile Met Val
251             240             245             250
253 acc cgt aag tta ggg gaa ggc ttc aag tct tta gag cca ggg tgg tac       879
254 Thr Arg Lys Leu Gly Glu Gly Phe Lys Ser Leu Glu Pro Gly Trp Tyr
255             255             260             265
257 tcc gcc atg gcc caa ggg caa gcc att tct aca tta gtc agg gcc tat       927
258 Ser Ala Met Ala Gln Gly Gln Ala Ile Ser Thr Leu Val Arg Ala Tyr
259 270             275             280             285
261 ctc tta aca aaa gac cat ata ttc ctc aat tca gct tta agg gca aca       975
262 Leu Leu Thr Lys Asp His Ile Phe Leu Asn Ser Ala Leu Arg Ala Thr
263             290             295             300
265 gcc cct tac aag ttt ctg tca gag cag cat gga gtc aag gct gtg ttt      1023
266 Ala Pro Tyr Lys Phe Leu Ser Glu Gln His Gly Val Lys Ala Val Phe
267             305             310             315
269 atg aat aaa cat gac tgg tat gaa gaa tat cca act aca cct agc tct      1071
270 Met Asn Lys His Asp Trp Tyr Glu Glu Tyr Pro Thr Thr Pro Ser Ser
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271        320                    325                330
273 ttt gtt tta aat ggc ttt atg tat tct tta att ggg ctg tat gac tta    1119
274 Phe Val Leu Asn Gly Phe Met Tyr Ser Leu Ile Gly Leu Tyr Asp Leu
275        335                    340                345
277 aaa gaa act gca ggg gaa aaa ctc ggg aaa gaa gcg agg tcc ttg tat    1167
278 Lys Glu Thr Ala Gly Glu Lys Leu Gly Lys Glu Ala Arg Ser Leu Tyr
279 350                    355                360                365
281 gag cgt ggc atg gaa tcc ctt aaa gcc atg ctc ccc ttg tac gac act    1215
282 Glu Arg Gly Met Glu Ser Leu Lys Ala Met Leu Pro Leu Tyr Asp Thr
283                    370                375                380
285 ggc tca gga acc atc tat gac ctc cgg cac ttc atg ctt ggc att gcc    1263
286 Gly Ser Gly Thr Ile Tyr Asp Leu Arg His Phe Met Leu Gly Ile Ala
287                    385                390                395
289 ccc aac ctg gcc cgc tgg gac tat cac acc acc cac atc aat caa ctg    1311
290 Pro Asn Leu Ala Arg Trp Asp Tyr His Thr Thr His Ile Asn Gln Leu
291                    400                405                410
293 cag ctg ctt agc acc att gat gag tcc cca atc ttc aaa gaa ttt gtc    1359
294 Gln Leu Leu Ser Thr Ile Asp Glu Ser Pro Ile Phe Lys Glu Phe Val
295        415                    420                425
297 aag agg tgg aag agc tac ctt aaa ggc agc cgg gca aag cac aac        1404
298 Lys Arg Trp Lys Ser Tyr Leu Lys Gly Ser Arg Ala Lys His Asn
299 430                    435                440
301 tagagctcag aaccaaaatc ctacgtcagc ctctgctgta cacagaaact agaggctctg    1464
303 tgtcagcaga gcataggcac attttaaaag gctgtatact aggttttttgt ggattacatc    1524
305 aaagtgataa atgatcctta aaaccagtct tctgagataa ttgcattcca tgggtttagt    1584
307 gtttagaatg tcgatggcat ttatagcaga aaagtgttta gtcagtgggc tgaatgaaga    1644
309 tgtttaactt ggcctcgctt atcaccctgt tcagttccac aggtagtcca gttctctcga    1704
311 tttgggaaag acaatggtaa gtagctcttg atggccagct gtccagcact tgtctgaaaa    1764
313 cttagtatgg ggctctttta aaatgtggtt atttatgttt atgttgaaag cagactttaa    1824
315 aaaaataatg tgctaaaata cagtaaatat gtacttgtag cctgatagtg actgtgtgca    1884
317 actttaaaaa tgattttttct tttctataaa ttaattttctt aggggtggat gagcatttgt    1944
319 tgtgtttgtt caagttgtta tatatggaga atattttgaa tttatgtttt gcttgaagtg    2004
321 tataaattaa aaacacaacc agtgttcagg cttcacagtt atataatgta agcacaacta    2064
323 aaatgaaact tgttgactgc acaagaaatt acaaaacaga acaaaaatgt tatctgttttt    2124
325 atgaaactat ctacaatcag taaagatttg ataatcagta tacccctcct gtaccccat    2184
327 tgtggtggtt tcttttttgcc actatctcaa attttgtatt tcatttcaga ctacacttga    2244
329 gagtttttgtc tatttttggggg ggacattttg gggacatttg ggaaattttta ctataaacct    2304
331 agatttgatg aggaggtagt aagtttaata agcccactac cactgccttt tctagattct    2364
333 tttccccttt aaggaaaaat attaggtcag atattataag gattgtagca gattttttttc    2424
335 ctacttagat cattcttggt ctacagcttt ccaaactatt gatgtacaca aaatacatag    2484
337 ttttttgtgta agctttcaaa cttttctggt gttttttttctt tgcagttttt aattttaaat    2544
339 tatttcagct cttggataaa agtgatgcta ctatattagc tgtacatgtg taatcagacc    2604
341 tttattttgg ttttatatcc cacatacctc acataaatag gcatcatagc cctcacaccc    2664
343 tgggcagtgt ctgctctagg acttaggcag taggtcagaa ctgagggagg ttgatttttgc    2724
345 tgtctctgtt ttagtgtatg acaatacagt aaatcaatac aataacttat acagattgga    2784
347 aatacgagat ccggtacttt cagaggactg agtctgacac acgcagtgca gtgtgtgtgt    2844
349 gacctgtatg aaatgcacat caagagcgag gtggcacctg cctgccactg catcttgcct    2904
351 ggacttagtc taccaacacc actcagaaat ggcaaaatgc atacatgcct ttgagcaaca    2964
353 tatatgttgt atcagcagcc ggaacgaaga cctacaactg acatgaaact gttagtcact    3024
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                    VERIFICATION SUMMARY              DATE: 04/30/2001
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                    Input Set : A:\Pto.amc
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L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:91 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:139 M:283 W: Missing Blank Line separator, <220> field identifier
L:146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
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